RAW SEQUENCE LISTING

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Application Serial Number: _09/836,544 C_
Source: _IFW16_
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ENTERED

IFW16

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 3 <110> APPLICANT: Seed, Brian
 4        Aruffo, Alejandro
 5        Camerini, David
 7 <120> TITLE OF INVENTION: CD27 Coding Sequence
 9 <130> FILE REFERENCE: 11-88L
11 <140> CURRENT APPLICATION NUMBER: US 09/836,544C
12 <141> CURRENT FILING DATE: 2001-04-17
14 <150> PRIOR APPLICATION NUMBER: US 07/983,647
15 <151> PRIOR FILING DATE: 1992-12-01
17 <150> PRIOR APPLICATION NUMBER: US 07/553,759
18 <151> PRIOR FILING DATE: 1990-07-13
20 <150> PRIOR APPLICATION NUMBER: US 07/498,809
21 <151> PRIOR FILING DATE: 1990-03-23
23 <150> PRIOR APPLICATION NUMBER: US 07/379,076
24 <151> PRIOR FILING DATE: 1989-07-13
26 <150> PRIOR APPLICATION NUMBER: US 07/160,416
27 <151> PRIOR FILING DATE: 1988-02-25
29 <160> NUMBER OF SEQ ID NOS: 37
31 <170> SOFTWARE: PatentIn Ver. 2.0
33 <210> SEQ ID NO: 1
34 <211> LENGTH: 2932
35 <212> TYPE: DNA
36 <213> ORGANISM: Artificial Sequence
38 <220> FEATURE:
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47 atactgtcct tctagtgtag ccgtagttag gccaccactt caagaactct gtagcaccgc 180
49 ctacatacct cgctctgcta atcctgttac cagtggctgc tgccagtggc gataagtcgt 240
51 gtcttaccgg gttggactca agacgatagt taccggataa ggcgcagcgg tcgggctgaa 300
53 cggggggttc gtgcacacag cccagcttgg agcgaacgac ctacaccgaa ctgagatacc 360
55 tacagcgtga gctatgagaa agcgccacgc ttcccgaagg agaaaggcg gacaggtatc 420
57 cggtaagcgg cagggtcgga acaggagagc gcacgaggga gcttccaggg ggaaacgcct 480
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61 gctcgtcagg ggggcggagc ctatggaaaa acgccagcaa cgccgaatta ccgcggtgtt 600
63 tctcaacgta acactttaca gcggcgcgtc atttgatatg atgcgccccg cttcccgata 660
65 agggagcagg ccagtaaaag cattacccgt ggtggggttc ccgagcggcc aaagggagca 720
67 gactctaaat ctgccgtcat cgacttcgaa ggttcgaatc cttcccccac caccatcact 780
69 ttcaaaagtc cgaaagaatc tgctccctgc ttgtgtgttg gaggtcgctg agtagtgcgc 840
71 gagtaaaatt taagctacaa caaggcaagg cttgaccgac aattgcatga agaatctgct 900
73 tagggttagg cgttttgcgc tgcttcgcga tgtacgggcc agatatacgc gttgacattg 960
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 77 ggagttccgc gttacataac ttacggtaaa tggcccgcct ggctgaccgc ccaacgaccc 1080
 79 ccgcccattg acgtcaataa tgacgtatgt tcccatagta acgccaatag ggactttcca 1140
 81 ttgacgtcaa tgggtggact atttacggta aactgcccac ttggcagtac atcaagtgta 1200
 83 tcatatgcca agtacgcccc ctattgacgt caatgacggt aaatggcccg cctggcatta 1260
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 89 ctcacgggga tttccaagtc tccaccccat tgacgtcaat gggagtttgt tttggcacca 1440
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113 gctttgctat ttacaccaca aaggaaaaag ctgcactgct atacaagaaa attatggaaa 2160
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133 ccagcaggca gaagtatgca aagcatgcat ctcaattagt cagcaaccat agtcccgccc 2760
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137 tgactaattt tttttattta tgcagaggcc gaggccgcct cggcctctga gctattccag 2880
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145 <213> ORGANISM: Homo sapiens
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149 <222> LOCATION: (7)..(1059)
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154         1               5                  10
156 ttc aat gtt tct tcc aaa ggt gca gtc tcc aaa gag att acg aat gcc     96
157 Phe Asn Val Ser Ser Lys Gly Ala Val Ser Lys Glu Ile Thr Asn Ala
158 15              20                  25                      30
160 ttg gaa acc tgg ggt gcc ttg ggt cag gac atc aac ttg gac att cct    144
161 Leu Glu Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro
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162                   35                  40                  45
164 agt ttt caa atg agt gat gat att gac gat ata aaa tgg gaa aaa act    192
165 Ser Phe Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr
166                   50                  55                  60
168 tca gac aag aaa aag att gca caa ttc aga aaa gag aaa gag act ttc    240
169 Ser Asp Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe
170              65                  70                  75
172 aag gaa aaa gat aca tat aag cta ttt aaa aat gga act ctg aaa att    288
173 Lys Glu Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile
174         80                  85                  90
176 aag cat ctg aag acc gat gat cag gat atc tac aag gta tca ata tat    336
177 Lys His Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr
178   95                  100                 105                 110
180 gat aca aaa gga aaa aat gtg ttg gaa aaa ata ttt gat ttg aag att    384
181 Asp Thr Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile
182                   115                 120                 125
184 caa gag agg gtc tca aaa cca aag atc tcc tgg act tgt atc aac aca    432
185 Gln Glu Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr
186              130                 135                 140
188 acc ctg acc tgt gag gta atg aat gga act gac ccc gaa tta aac ctg    480
189 Thr Leu Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu
190         145                 150                 155
192 tat caa gat ggg aaa cat cta aaa ctt tct cag agg gtc atc aca cac    528
193 Tyr Gln Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His
194   160                 165                 170
196 aag tgg acc acc agc ctg agt gca aaa ttc aag tgc aca gca ggg aac    576
197 Lys Trp Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn
198 175                 180                 185                 190
200 aaa gtc agc aag gaa tcc agt gtc gag cct gtc agc tgt cca gag aaa    624
201 Lys Val Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys
202                   195                 200                 205
204 ggt ctg gac atc tat ctc atc att ggc ata tgt gga gga ggc agc ctc    672
205 Gly Leu Asp Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Gly Ser Leu
206              210                 215                 220
208 ttg atg gtc ttt gtg gca ctg ctc gtt ttc tat atc acc aaa agg aaa    720
209 Leu Met Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Lys Arg Lys
210         225                 230                 235
212 aaa cag agg agt cgg aga aat gat gag gag ctg gag aca aga gcc cac    768
213 Lys Gln Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His
214   240                 245                 250
216 aga gta gct act gaa gaa agg ggc cgg aag ccc cac caa att cca gct    816
217 Arg Val Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala
218 255                 260                 265                 270
220 tca acc cct cag aat cca gca act tcc caa cat cct cct cca cca cct    864
221 Ser Thr Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Pro
222                   275                 280                 285
224 ggt cat cgt tcc cag gca cct agt cat cgt ccc ccg cct cct gga cac    912
225 Gly His Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His
226              290                 295                 300
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RAW SEQUENCE LISTING   DATE: 10/14/2005
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229 Arg Val Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr
230         305             310             315
232 caa gtt cac cag cag aaa ggc ccg ccc ctc ccc aga cct cga gtt cag  1008
233 Gln Val His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln
234         320             325             ·330
236 cca aaa cct ccc cat ggg gca gca.gaa aac tca ttg tcc cct tcc tct  1056
237 Pro Lys Pro Pro His Gly Ala Ala Glu Asn Ser Leu Ser Pro Ser Ser
238 335             340             345             350
240 aat taaaaaagat agaaactgtc tttttcaata aaaagcactg tggatttctg        1109
241 Asn
243 ccctcctgat gtgcatatcc gtacttccat gaggtgtttt ctgtgtgcag aacattgtca 1169
245 cctcctgagg ctgtgggcca cagccacctc tgcatcttcg aactcagcca tgtggtcaac 1229
247 atctggagtt tttggtctcc tcagagagct ccatcacacc agtaaggaga agcaatataa 1289
249 gtgtgattgc aagaatggta gaggaccgag cacagaaatc ttagagattt cttgtcccct 1349
251 ctcaggtcat gtgtagatgc gataaatcaa gtgattggtg tgcctgggtc tcactacaag 1409
253 cagcctatct gcttaagaga ctctggagtt tcttatgtgc cctggtggac acttgcccac 1469
255 catcctgtga gtaaaagtga aataaaagct ttgac                            1504
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260 <212> TYPE: PRT
261 <213> ORGANISM: Homo sapiens
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267 Val Ser Ser Lys Gly Ala Val Ser Lys Glu Ile Thr Asn Ala Leu Glu
268             20              25              30
270 Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro Ser Phe
271 .       35              40              45
273 Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr Ser Asp
274         50              55                  60
276 Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe Lys Glu
277 65                  70                  75                  80
279 Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile Lys His
280             85              90              95
282 Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr Asp Thr
283         100             105             110
285 Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile Gln Glu
286         115             120             125
288 Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr Thr Leu
289     130             135             140
291 Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu Tyr Gln
292 145             150             155             160
294 Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His Lys Trp
295             165             170             175·
297 Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn Lys Val
298             180             185             190
300 Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys Gly Leu
301             195             200             205
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306 Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Lys Arg Lys Lys Gln
307 225             230             235             240
309 Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His Arg Val
310             245             250             255
312 Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala Ser Thr
313             260             265             270
315 Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Gly His
316         275             280             285
318 Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His Arg Val
319     290             295             300
321 Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr Gln Val
322 305             310             315             320
324 His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln Pro Lys
325             325             330             335
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345 ctc agc gtg gtc tgc ctg ctg cac tgc ttt ggt ttc atc agc tgt ttt  99
346 Leu Ser Val Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe
347     15              20              25
349 tcc caa caa ata tat ggt gtt gtg tat ggg aat gta act ttc cat gta  147
350 Ser Gln Gln Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val
351 30              35              40              45
353 cca agc aat gtg cct tta aaa gag gtc cta tgg aaa aaa caa aag gat  195
354 Pro Ser Asn Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp
355             50              55              60
357 aaa gtt gca gaa ctg gaa aat tct gaa ttc aga gct ttc tca tct ttt  243
358 Lys Val Ala Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe
359             65              70              75
361 aaa aat agg gtt tat tta gac act gtg tca ggt agc ctc act atc tac  291
362 Lys Asn Arg Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr
363             80              85              90
365 aac tta aca tca tca gat gaa gat gag tat gaa atg gaa tcg cca aat  339
366 Asn Leu Thr Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn
367     95              100             105
369 att act gat acc atg aag ttc ttt ctt tat gtg ctt gag tct ctt cca  387
370 Ile Thr Asp Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro
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VERIFICATION SUMMARY　　　　　　　　　DATE: 10/14/2005
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